



SEQUENCE LISTING

<110> Astra Aktiebolag

<120> Vaccine Delivery System and Method of Production

<130> 1103326-0560

<140> 09/308,435

<141> 1999-05-19

<150> PCT/SE99/00582

<151> 1999-04-09

<150> SE 9801288-3

<151> 1998-04-14

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 1670

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (793) .. (1572)

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gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgcccc 180
aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaatcaa ctaaaaatgg 240
tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
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aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
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 acgctaataaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
 Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
 1 5 10
 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
 15 20 25
 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
 30 35 40 45
 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
 50 55 60
 agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
 Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
 65 70 75
 aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat 1071
 Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn
 80 85 90
 caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
 Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
 95 100 105
 tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
 Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
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 gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
 Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
 130 135 140
 gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
 Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
 145 150 155

tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
 Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
 160 165 170

ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
 Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
 175 180 185

caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
 Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
 190 195 200 205

gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
 Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
 210 215 220

agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
 Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
 225 230 235

aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
 Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
 240 245 250

tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602
 Leu Lys Gly Lys Arg Asn Arg
 255 260

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tgatgatc 1670

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<211> 260

<212> PRT

<213> *Helicobacter pylori*

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Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
 1 5 10 15

Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
 20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
 35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
50 55 60

Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
65 70 75 80

Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
85 90 95

Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
100 105 110

Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
115 120 125

Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
130 135 140

Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
145 150 155 160

Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
165 170 175

Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
180 185 190

Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
195 200 205

Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
210 215 220

Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
225 230 235 240

Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
245 250 255

Lys Arg Asn Arg
260

<210> 3

<211> 1670

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (793)..(1572)

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gatttgattt tagggaatta catgcaagtg aatgaaaaaa acattcaagc gtttgccccc 180

aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaatcaa cctaaaatgg 240

tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300

tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360

aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420

gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480

gttttaaaact ctatgcgaga gtcaaaactc aagctaaaac gggcgtagaa atggaagcgc 540

taatgagtgt gagcgtaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600

gcatgacaat tagcgggtgtg atgctggaat ataaaagtgg aggcaaaagt ggggattata 660

acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720

caacaaaagc gtgttggttg cttcggtttt gttgttatag aagtctaaaa tattacaatc 780

aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831

Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys

1

5

10

aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879

Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser

15

20

25

ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927

Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His

30

35

40

45

cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975

Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu

50

55

60

agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac	1023
Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn	
65 70 75	
aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat	1071
Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn	
80 85 90	
caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt	1119
Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe	
95 100 105	
tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc	1167
Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly	
110 115 120 125	
gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca	1215
Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser	
130 135 140	
gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt	1263
Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val	
145 150 155	
tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt	1311
Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser	
160 165 170	
ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att	1359
Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile	
175 180 185	
caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta	1407
Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu	
190 195 200 205	
gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag	1455
Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys	
210 215 220	
aga gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa	1503
Arg Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys	
225 230 235	
aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa	1551
Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu	
240 245 250	

tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602
 Leu Lys Gly Lys Arg Asn Arg
 255 260

cttgaataaaa ctgcttaaaaa aggggtttttt agcggttcttt ttgagcgtgt atttaagggc 1662
 tgatgatc 1670

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 Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
 20 25 30
 Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
 35 40 45
 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
 50 55 60
 Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
 65 70 75 80
 Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
 85 90 95
 Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
 100 105 110
 Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
 115 120 125
 Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
 130 135 140
 Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
 145 150 155 160
 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
 165 170 175

Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
180 185 190

Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
195 200 205

Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu
210 215 220

Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
225 230 235 240

Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
245 250 255

Lys Arg Asn Arg
260

<210> 5
<211> 60
<212> PRT
<213> Helicobacter pylori

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1 5 10 15

Leu Gly Thr Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
50 55 60

<210> 6
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<213> Helicobacter pylori

<400> 6
Met Lys Thr Asn Gly His Phe Lys Asp Phe Ala Trp Lys Lys Cys Phe
1 5 10 15

Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
50 55 60

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1 5 10 15

Leu Gly Ala Ser Val Gly Ala Leu Leu Val Gly Cys Ser Pro His Ile
20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
50 55 60

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<213> Helicobacter pylori

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Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
50 55 60

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 <213> Helicobacter pylori

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 20 25 30
 Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
 35 40 45
 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
 50 55 60

<210> 10
 <211> 60
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 <213> Helicobacter pylori

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 1 5 10 15
 Asn Lys Phe Lys Asn Gln Thr Thr Leu Lys Val Glu Glu Ile Leu Gln
 20 25 30
 Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser Asp Lys Asp Asp
 35 40 45
 Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
 50 55 60

<210> 11
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 11
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 1 5 10 15

Asn Lys Phe Lys Asn Gln Thr Thr Leu Lys Val Glu Glu Ile Leu Gln
20 25 30

Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser Asp Lys Asp Asp
35 40 45

Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
50 55 60

<210> 12

<211> 60

<212> PRT

<213> *Helicobacter pylori*

<400> 12

Leu Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu
1 5 10 15

Asn Lys Phe Lys Asn Gln Thr Val Leu Lys Val Glu Gln Ile Leu Gln
20 25 30

Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser Asp Lys Asp Asp
35 40 45

Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
50 55 60

<210> 13

<211> 60

<212> PRT

<213> *Helicobacter pylori*

<400> 13

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1 5 10 15

Asn Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln
20 25 30

Asn Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp
35 40 45

Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
50 55 60

<210> 14
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 14
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 1 5 10 15
 Asn Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln
 20 25 30
 Asn Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp
 35 40 45
 Leu Ser Phe Ser Gln Lys Lys Glu Gly Tyr Leu Ala
 50 55 60

<210> 15
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 15
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 1 5 10 15
 Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp
 20 25 30
 Lys Met Glu Gly Val Leu Ile Pro Ala Gly Phe Val Lys Val Thr Ile
 35 40 45
 Leu Glu Pro Met Ser Gly Glu Ser Leu Asp Ser Phe
 50 55 60

<210> 16
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 16
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 1 5 10 15
 Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp

	20		25		30
Lys Met Glu Gly Val Leu Ile Pro Ala Gly Phe Val Lys Val Thr Ile					
	35		40		45

Leu Glu Pro Met Ser Gly Glu Ser Leu Asp Ser Phe
50 55 60

<210> 17
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 <212> PRT
 <213> Helicobacter pylori

<400> 17
Val Ala Met Asn Gly Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr
1 5 10 15

Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp
20 25 30

Lys Met Glu Gly Val Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile
35 40 45

Leu Glu Pro Met Ser Gly Glu Ser Leu Asp Ser Phe
50 55 60

<210> 18
 <211> 60
 <212> PRT
 <213> Helicobacter pylori

<400> 18
Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys Phe Leu Lys Thr
1 5 10 15

Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr Met Val Lys Gly
20 25 30

Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe
35 40 45

Ala Ser Ile Met Gln Glu Met Asp Lys Lys Leu Thr
50 55 60

<210> 19

<212> PRT

<213> Helicobacter pylori

<400> 19

<210> 20

<211> 60

<212> PRT

<213> Helicobacter pylori

<400> 20

Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys Phe Leu Lys Thr
1 5 10 15

Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr Met Val Lys Gly
20 25 30

Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe
35 40 45

Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
50 55 60

<210> 21

<211> 20

<212> PRT

<213> Helicobacter pylori

<400> 21

Gln Arg Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Asn
1 5 10 15

Lys Arg Asn Arg
20

<210> 22

<211> 20

<212> PRT

<213> Helicobacter pylori

<400> 22

Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu Leu Lys Gly
1 5 10 15

Lys Arg Asn Arg
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<210> 23
<211> 31
<212> PRT
<213> Helicobacter pylori

<400> 23
Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys Lys Cys Leu
1 5 10 15

Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Leu Ala Gly Cys
20 25 30

<210> 24
<211> 31
<212> PRT
<213> Helicobacter pylori

<220>
<221> MOD_RES
<222> (31)
<223> n-propyl alcohol attached to sulfhydryl group of
cysteine residue at position 31

<400> 24
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1 5 10 15

Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Leu Ala Gly Cys
20 25 30

<210> 25
<211> 31
<212> PRT
<213> Helicobacter pylori

<220>
<221> MOD_RES
<222> (31)
<223> lipid chains a and b attached respectively at
positions 3 and 2 of propyl group attached to
sulfhydryl of cysteine residue at position 31

<400> 25

Met	Arg	Ala	Asn	Asn	His	Phe	Lys	Asp	Phe	Ala	Trp	Lys	Lys	Cys	Leu
1				5					10					15	

Leu	Gly	Ala	Ser	Val	Val	Ala	Leu	Leu	Val	Gly	Leu	Ala	Gly	Cys	
			20					25						30	



(1993) J. Bacteriol. 175, 674-683. Reference is also made to P W Toole *et al*, Bacteriology Vol. 177, No. 21, Nov. 1995; and Jones, A.C., Logan, R.P., Foynes, S., Cockayne, A., Wren, B.W. and Penn, C.W., J. Bacteriol. 179 (17), 5643-5647 (1997) which concern HpaA proteins.

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The Hpa A protein is expressed by all *H. pylori* strains tested, and antibodies created towards this protein do not cross-react with common endogenous human bacteria of other species or with selected human tissues including the gastric mucosa. Thus being a well conserved putative adhesin with immunogenic properties, the HpaA protein is useful both for the detection of *H. pylori* infections as well as for the manufacture of vaccine compositions. Table 1 shows a comparison of HpaA amino acid sequences derived from 4 different strains of *H. Pylori*. It can be seen from the table that the sequence is highly conserved amongst different strains.

15 Table 1

Evans (8826)	MKTNGHFKDFAWKKCLLGTSVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:5)
GTC (J99)	MKTNGHFKDFAWKKCFLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:6)
Trust (17874)	MKTNGHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:7)
20 Penn (11637)	MRANNHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:8)
TIGR (26695)	MKANNHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:9)
	.**.***
Evans (8826)	LKPAFYSDNIAKEYENKFKNQTTLKVEEILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:10)
25 GTC (J99)	LRPAFYSDNIAKEYENKFKNQTTLKVEEILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:11)
Trust (17874)	LRPAFYSDNIAKEYENKFKNQTVLKVEQILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:12)
Penn (11637)	LRPAFYSDNIAKEYENKFKNQTTALKVEQILQNQGYKVISVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:13)
TIGR (26695)	LRPAFYSDNIAKEYENKFKNQTTALKVEQILQNQGYKVISVDSSDKDDLSFSQKKEGYLA (SEQ ID NO:14)
	.**.***

Evans (8826)	VAMIGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF (SEQ ID NO:15)
GTC (J99)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF (SEQ ID NO:16)
Trust (17874)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF (SEQ ID NO:16)
Penn (11637)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFIKVTILEPMSGESLDSF (SEQ ID NO:17)

TIGR (26695) VAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF (SEQ ID NO:16)

.....

Evans (8826) TMDLSELDIQEKFLKTTSSSHSGGLVSTMVKGTDNSNDAIKSALNKIFASIMQEMDKKLT (SEQ ID NO:18)

5 GTC (J99) TMDLSELDIQEKFLKTTSSSHSGGLVSTMVKGTDNSNDAIKSALNKIFASIMQEMDKKLT (SEQ ID NO:18)

Trust (17874) TMDLSELDIQEKFLKTTSSSHSGGLVSTMVKGTDNSNDAIKSALNKIFGSIMQEIDKKLT (SEQ ID NO:19)

Penn (11637) TMDLSELDIQEKFLKTTSSSHSGGLVSTMVKGTDNSNDAIKSALNKIFANIMQEIDKKLT (SEQ ID NO:20)

TIGR (26695) TMDLSELDIQEKFLKTTSSSHSGGLVSTMVKGTDNSNDAIKSALNKIFANIMQEIDKKLT (SEQ ID NO:20)

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Evans (8826) QRNLESYQKDAKELKNKRN (SEQ ID NO:21)

GTC (J99) QRNLESYQKDAKELKNKRN (SEQ ID NO:21)

Trust (17874) QKNLESYQKDAKELKGKRN (SEQ ID NO:22)

Penn (11637) QKNLESYQKDAKELKGKRN (SEQ ID NO:22)

15 TIGR (26695) QKNLESYQKDAKELKGKRN (SEQ ID NO:22)

..:.....

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20 type such as lysine or arginine at a certain position).

Penn (11637) DNA sequence deposited in Genbank under Accession No. X92502

Trust (17874) DNA sequence deposited in Genbank under Accession No.U35455

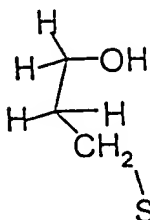
Evans (8826) DNA sequence deposited in Genbank under Accession No.X61574

25 TIGR (26695) DNA sequence deposited under Accession No. AE000591

GTC (J99) DNA sequence obtained in-house.

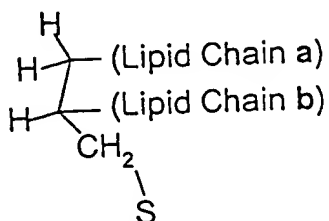
The strain names are indicated in brackets, strain 8826 being obtained from SWISS-PROT accession Q48264.

I Met — Leu-Ala-Gly-Cys — Protein (SEQ ID NO:23)



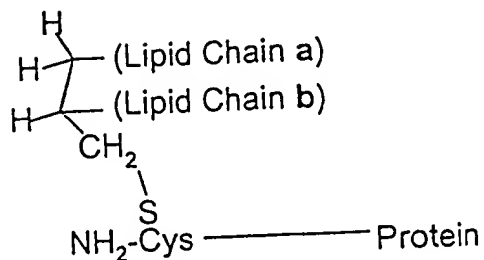
II Met — Leu-Ala-Gly-Cys — Protein (SEQ ID NO:24)

III

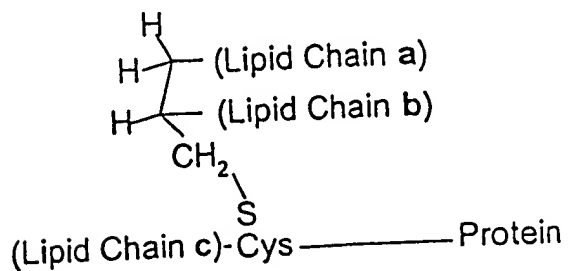


Met — Leu-Ala-Gly-Cys — Protein (SEQ ID NO:25)

IV



V





(1993) J. Bacteriol. 175, 674-683. Reference is also made to P W Toole *et al*, Bacteriology Vol. 177, No. 21, Nov. 1995; and Jones, A.C., Logan, R.P., Foynes, S., Cockayne, A., Wren, B.W. and Penn, C.W., J. Bacteriol. 179 (17), 5643-5647 (1997) which concern HpaA proteins.

5

The Hpa A protein is expressed by all *H. pylori* strains tested, and antibodies created towards this protein do not cross-react with common endogenous human bacteria of other species or with selected human tissues including the gastric mucosa. Thus being a well conserved putative adhesin with immunogenic properties, the HpaA protein is useful both for the detection of *H. pylori* infections as well as for the manufacture of vaccine compositions. Table 1 shows a comparison of HpaA amino acid sequences derived from 4 different strains of *H. Pylori*. It can be seen from the table that the sequence is highly conserved amongst different strains.

Table 1

Evans (8826)	MKTNGHFKDFAWKKCLLGTSVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:5)
GTC (J99)	MKTNGHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:6)
Trust (17874)	MKTNGHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:7)
Penn (11637)	MRANNHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:8)
TIGR (26695)	MKANNHFKDFAWKKCLLGASVVALLVGCSPHIETNEVALKLNYPASEKVQALDEKILL (SEQ ID NO:9)
::.*****:~::~*****	
Evans (8826)	LKPAFYSDNIAKEYENKFKNQTTLKVEEILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:10)
GTC (J99)	LRPAFYSDNIAKEYENKFKNQTTLKVEEILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:11)
Trust (17874)	LRPAFYSDNIAKEYENKFKNQTVLKVEQILQNQGYKVINVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:12)
Penn (11637)	LRPAFYSDNIAKEYENKFKNQTTALKVEQILQNQGYKVISVDSSDKDDFSFAQKKEGYLA (SEQ ID NO:13)
TIGR (26695)	LRPAFYSDNIAKEYENKFKNQTTALKVEQILQNQGYKVISVDSSDKDDLSFSQKKEGYLA (SEQ ID NO:14)
*::*****:~::~*****	

Evans (8826)	VAMIGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF	(SEQ ID NO:15)
GTC (J99)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF	(SEQ ID NO:16)
Trust (17874)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFVKVTILEPMSGESLDSF	(SEQ ID NO:16)
Penn (11637)	VAMNGEIVLRPD?KRTIQKKSEPGLLFSTGLDKMEGVLPAGFIKVTILEPMSGESLDSF	(SEQ ID NO:17)

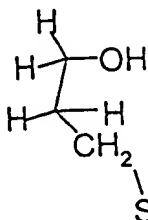
	TIGR (26695)	VAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFVKVTILEPMSGESLDSF (SEQ ID NO:16)
	
	Evans (8826)	TMDLSELDIQEKFLKTTTHSSHSGLVSTMVKGTDNSNDAIKSALNKIFASIMQEMDKKLT (SEQ ID NO:18)
5	GTC (J99)	TMDLSELDIQEKFLKTTTHSSHSGLVSTMVKGTDNSNDAIKSALNKIFASIMQEMDKKLT (SEQ ID NO:18)
	Trust (17874)	TMDLSELDIQEKFLKTTTHSSHSGLVSTMVKGTDNSNDAIKSALNKIFGSIMQEIDKKLT (SEQ ID NO:19)
	Penn (11637)	TMDLSELDIQEKFLKTTTHSSHSGLVSTMVKGTDNSNDAIKSALNKIFANIMQEIDKKLT (SEQ ID NO:20)
	TIGR (26695)	TMDLSELDIQEKFLKTTTHSSHSGLVSTMVKGTDNSNDAIKSALNKIFANIMQEIDKKLT (SEQ ID NO:20)
	
10		
	Evans (8826)	QRNLESYQKDAKELKNKRN (SEQ ID NO:21)
	GTC (J99)	QRNLESYQKDAKELKNKRN (SEQ ID NO:21)
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	Penn (11637)	QKNLESYQKDAKELKGKRN (SEQ ID NO:22)
15	TIGR (26695)	QKNLESYQKDAKELKGKRN (SEQ ID NO:22)
	

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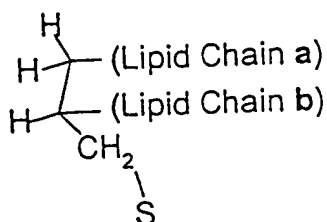
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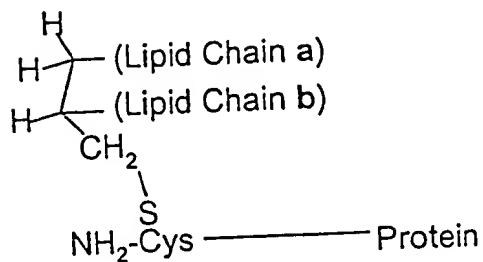
II Met — Leu-Ala-Gly-Cys — Protein (SEQ ID NO:24)

III



Met — Leu-Ala-Gly-Cys — Protein (SEQ ID NO:25)

IV



V

